

Figure 1. 158P1D7 SSH sequence (SEQ ID NO:655).

```
1 GATCTGATAA GCTTTCAATG TTGCGCTCCT GACAATGTAT TAGAAGTCCT GATGGGGATA
61 GGACTTTGCA GTTACAAGGA ATAGGGCAGA AAGGTCCTGG AAGTTGAGTG GATGGCTTTG
121 TAATATAAGG TATCAAACCT GGTGCTTTGG TGGGTAGTTT TAGAATGGAC GTGGTCTTAG
181 TTGACATGCG ACTATCATT ATTGAAGATG TTGCTGCCAG ATGTAATGAT C
```

Figure 1

Figure 2. 158P1D7 cDNA clone TurboScript3PX and open reading frame (ORF)

1 M K L W I H L F Y S S L L
1 tcggattttcatcacatgacaacATGAAGCTGTGGATTTCATCTCTTTTATTTCATCTCTCCT
14 A C I S L H S Q T P V L S S R G S C D S
61 TGCCTGTATATCTTTACACTCCCAAACCTCCAGTGCCTCTCATCCAGAGGCTCTTGTGATTG
34 L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54 K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTA
74 N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94 H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTAAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACCTTCATATCAATCACAATTCCTTTAGAAAATCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTGTGTTCTTTAACCCTATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D C T
601 TCAATTACAAACATTGCCTTATGTTGGTTCCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTGCATGTCAACTAAGACCACGTCCATTCTAAAACCTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCCATCCCCATCAGGACTTCTAATACATTGTGAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGAAAATCCTAGAAAGCTCATTCTAGCGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCCTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTCTGG
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATTTTTGGATGATCTTGATTACTAACCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q

1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTACTGAAAGACC
674 S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694 S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
714 A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAAACAGGAAAATCATTCACTCACAGGGTC
734 N M K Y K T T N Q S T E F L S F Q D A S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
754 S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA
774 Y L R K N I A Q L Q P D M E A H Y P G A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794 H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814 E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAATGAGTATTTTGAACCTAAAGCTAATTTACATGCTGAACCTGACTA
834 L E V L E Q Q T * (SEQ ID NO:657)
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga (SEQ ID NO:656)

Figure 3. 158P1D7 amino acid sequence.

```
1 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEP S AFSKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNPMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDDLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ H MVSPMVHVY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS
721 LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA
781 QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ
841 T* (SEQ ID NO:657)
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158P1D7

Figure 4. 158PID7 amino acid BLAST homology to hypothetical protein RLJ22114.

Identities = 798/798 (100%)

Query: 44 MLINCEAKGIKVMSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
 MLINCEAKGIKVMSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADI
 Sbjct: 1 MLINCEAKGIKVMSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

Query: 104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
 Sbjct: 61 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

Query: 164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLLEDNKWACN 223
 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLLEDNKWACN
 Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLLEDNKWACN 180

Query: 224 CDLLQLKWTLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 283
 CDLLQLKWTLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL
 Sbjct: 181 CDLLQLKWTLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 240

Query: 284 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
 Sbjct: 241 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344 LIHCQERNIESLSDLRPPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRIEVL 403
 LIHCQERNIESLSDLRPPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRIEVL
 Sbjct: 301 LIHCQERNIESLSDLRPPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRIEVL 360

Query: 404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 463
 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV
 Sbjct: 361 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 420

Query: 464 LYLNNNLLQVLPPIHFGVPLTKVNLKTNQFTHLPVSNILDDDLLTQIDLEDNPWDCSC 523
 LYLNNNLLQVLPPIHFGVPLTKVNLKTNQFTHLPVSNILDDDLLTQIDLEDNPWDCSC
 Sbjct: 421 LYLNNNLLQVLPPIHFGVPLTKVNLKTNQFTHLPVSNILDDDLLTQIDLEDNPWDCSC 480

Query: 524 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM 583
 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM
 Sbjct: 481 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM 540

Query: 584 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 643
 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ
 Sbjct: 541 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 600

Query: 644 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 703
 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE
 Sbjct: 601 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 660

Query: 704 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 763
 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE
 Sbjct: 661 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 720

Query: 764 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 823
 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL
 Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 780

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS

First Inventor: Mary FARIS, et al.

Application No.: To be assigned

Docket No.: 51158-20050.00

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Query: 824 KANLHAEPDYLEVLEQQT 841

KANLHAEPDYLEVLEQQT

Sbjct: 781 KANLHAEPDYLEVLEQQT 798 (SEQ ID NO:658)

TOEBO: 0E7H3E660

Figure 5a: Alignment of 158P1D7 with human FLJ22774, CLONE KAIA1575. [Homo sapiens]

Identities = 405/415 (97%), Positives = 405/415 (97%)

```

158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPQNPRLILAGNIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 403
              LIHCQERNIESLSDLRPPQNPRLILAGNIHSLMKSDLVEYFTLEMLHLGNNRIEVLE
Sbjct: 301    LIHCQERNIESLSDLRPPQNPRLILAGNIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 360

158P1D7:404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458
              EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLH                      AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHLELYLYEYNAIKEILPGTFNPM 415 (SEQ ID
NO:659)

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Figure 5b: Alignment of 158P1D7 protein with a human protein similar to IGFALS

Identities = 316/864 (36%), Positives = 459/864 (52%)

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158P1D7:1  MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEIS 60
              M LW+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17   MFLWLFLILSALISSTNADSDISV-----EICNVCSCSVENVLYVNCVKSVYRPNQLK 71

158P1D7:61  VPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFGNNIADIEIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72   PPWSNFYHLNFQNNFLNILYPNTFLNFHAVSLHLGNNKLQNIEGGAFGLSALKQLHLN 131

158P1D7:121 HNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVILNDN I LP NIF
Sbjct: 132  NNELKILRADTFGLIENLEYLQADYNLIKYIERGAFNKLHLKVLILNDNLISFLPDNIF 191

158P1D7:181 RFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192  RFASLTHLDIRGNRIQKLPIYGVLEHIGRVVELQLEDNPWNCSCDLLPLKAWLENMPYNI 251

158P1D7:241 IIGDVVCNSPPFFKGSILSRLKKEICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252  YIGEACETPSDLYGRLLKETNKQELCPMGTGSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290 SINDSRMSTKTTSSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPICNCKV- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312  LHRLVTKPPKTTN---PSKISGIVAGKALSNNRNLISQIVSYQTRVPPLTPCPAPCFCKTH 367

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158P1D7:338 LSPSGLLIHCQERNIESLSDLRPPPPQNPRKLILAGNIIHSLMKSDDLVEYFTLEMLHLGNN 397
S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368 PSDLGLSVNCQEKNIQSMSELIPKPLNAKLHVNGNSIKDVDVSDFTDFEGLDLLHLGNS 427

158P1D7:398 RIEVLEEGSFMNLTRELQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNP 457
+I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+
Sbjct: 428 QITVIKGDVFNLTNLRLRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

158P1D7:458 MXXXXXXXXXXXXXXXXXXXXHIFSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N
Sbjct: 488 MPNLQLLYLNNLLKSLPVYIFSGAPLARLNLNRNKFMYLPVSGVLDQLQSLTQIDLEG 547

158P1D7:518 PWDSCDLVGLQWQIQLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPT 577
PWD+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P
Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +
Sbjct: 607 ---FTSPAPAITFTTLPGLPIRSPPGGPVPLSILILSVLVLILTVFVAFCLLVFVLRNK 663

158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHMVSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G
Sbjct: 664 KPTVKHEGLGNPDCGSMQLQLRKHDH-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +
Sbjct: 719 KESETGFMFSDPPGQ--KVVMRNVADKEKDLLHVDTRKRLSTIDELDELFPSSRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKKSKSLIGGNHISKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841
+EYFELKA L + PDYL+VLE+QT
Sbjct: 825 SEYFELKAKLQSSPDYLQVLEEQT 848 (SEQ ID NO:660)

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
First Inventor: Mary FARIS, et al.
Application No.: To be assigned
Docket No.: 51158-20050.00
Sheet 8 of 20

Figure 6. Expression of 158P1D7 by RT-PCR

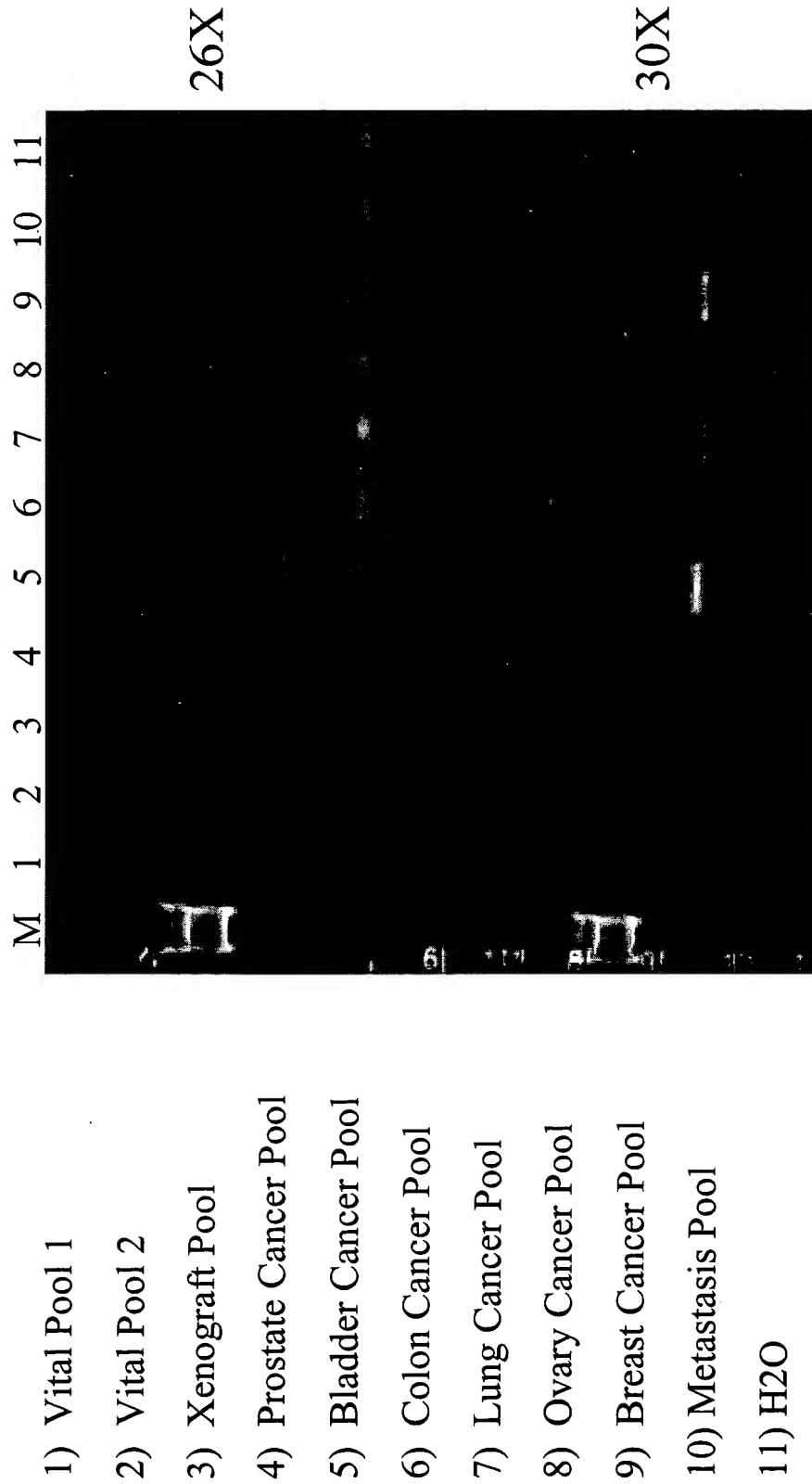


Figure 7. Expression of 158P1D7 in Normal Tissues

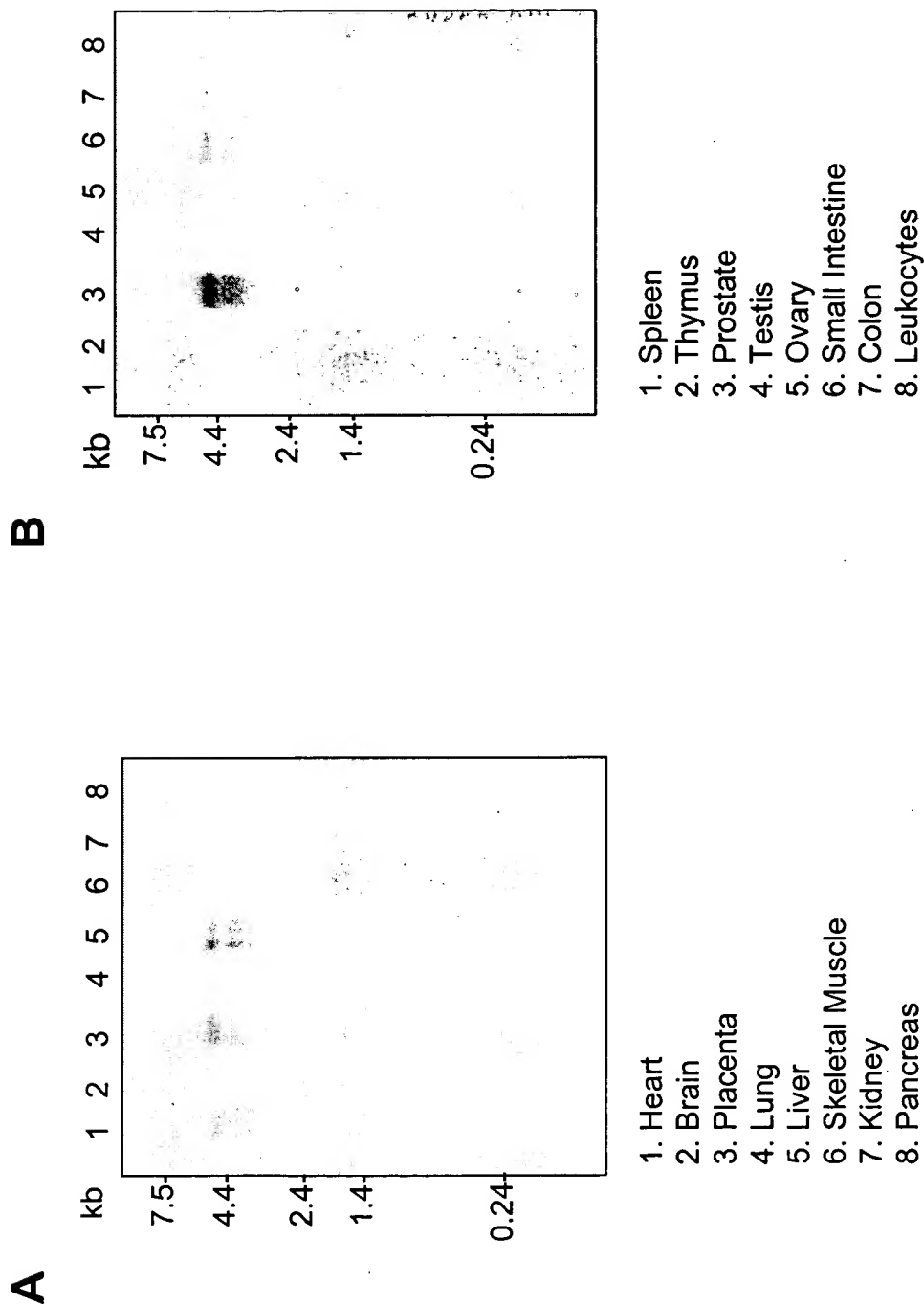
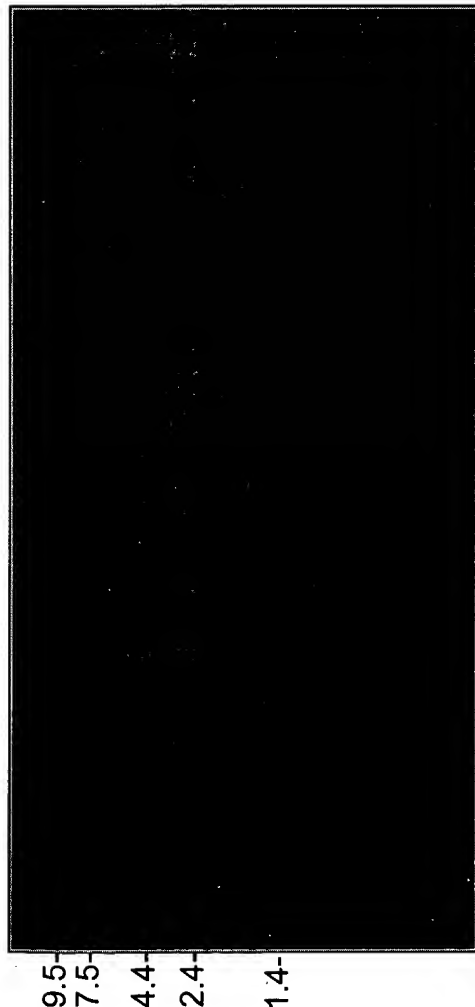


Figure 8A. Expression of 158P1D7 in Bladder Cancer Patient Specimens

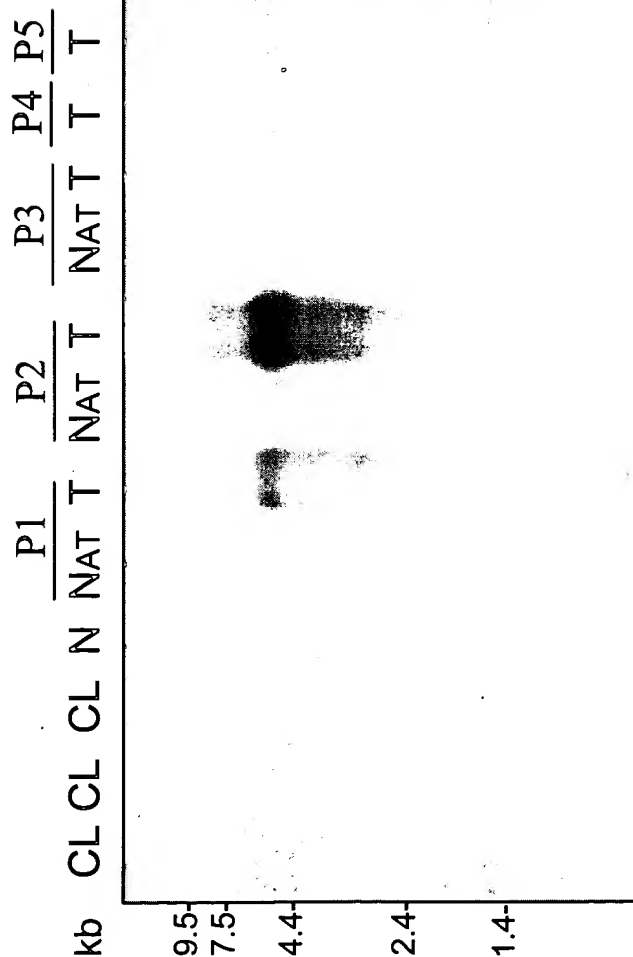
kb CL CL CL N NAT T NAT T P1 P2 P3 P4 P5 P6
T T T T T T T T T T T T T



P1 - Transitional, grade 4
P2 - Squamous inv.
P3 - Transitional, grade 3
P4 - Papillary non-inv, grade 1/3
P5 - Papillary, grade 3/3
P6 - Transitional, grade 3/2

CL = Cell lines (listed in order): UM-UC-3, J82, SCaBER
P = Patient
N = Normal Bladder
NAT = Normal adjacent tissue
T = Tumor

Figure 8B. Expression of 158P1D7 in Bladder Cancer Patient Specimens



P1 - Transitional, grade 2
 P2 - Transitional, grade 3/2
 P3 - Transitional,
 P4 - Polypoid Cystitis
 P5 - Papillary, grade 3/3

Figure 9. Expression of 158P1D7 in Lung Cancer Patient Specimens

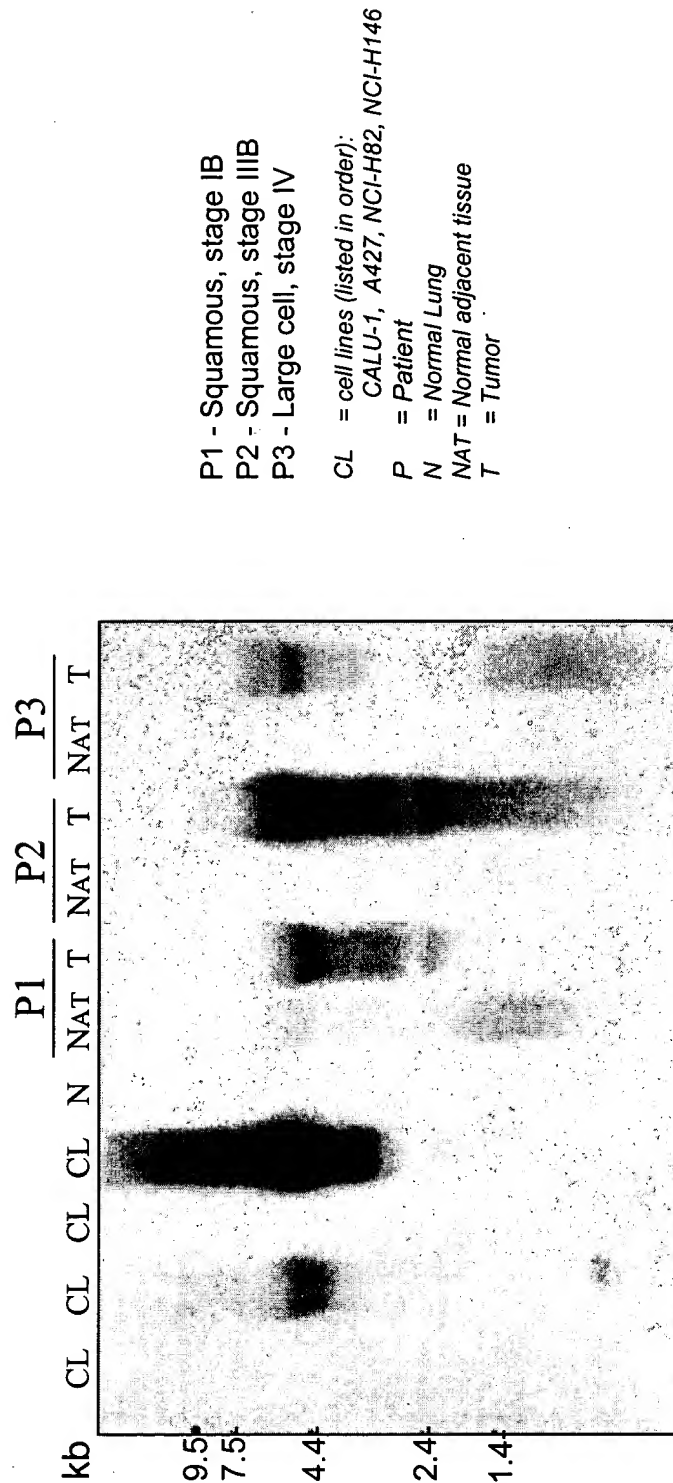


Figure 10. Expression of 158P1D7 in Breast Cancer Patient Specimens

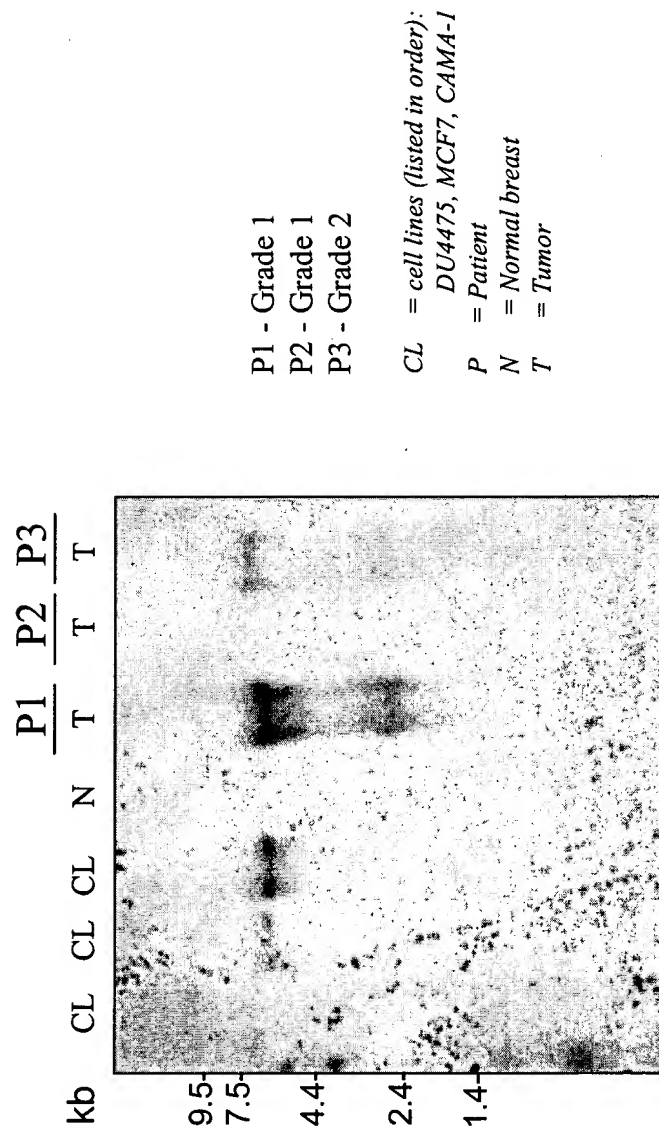


Figure 11. 158P1D7 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

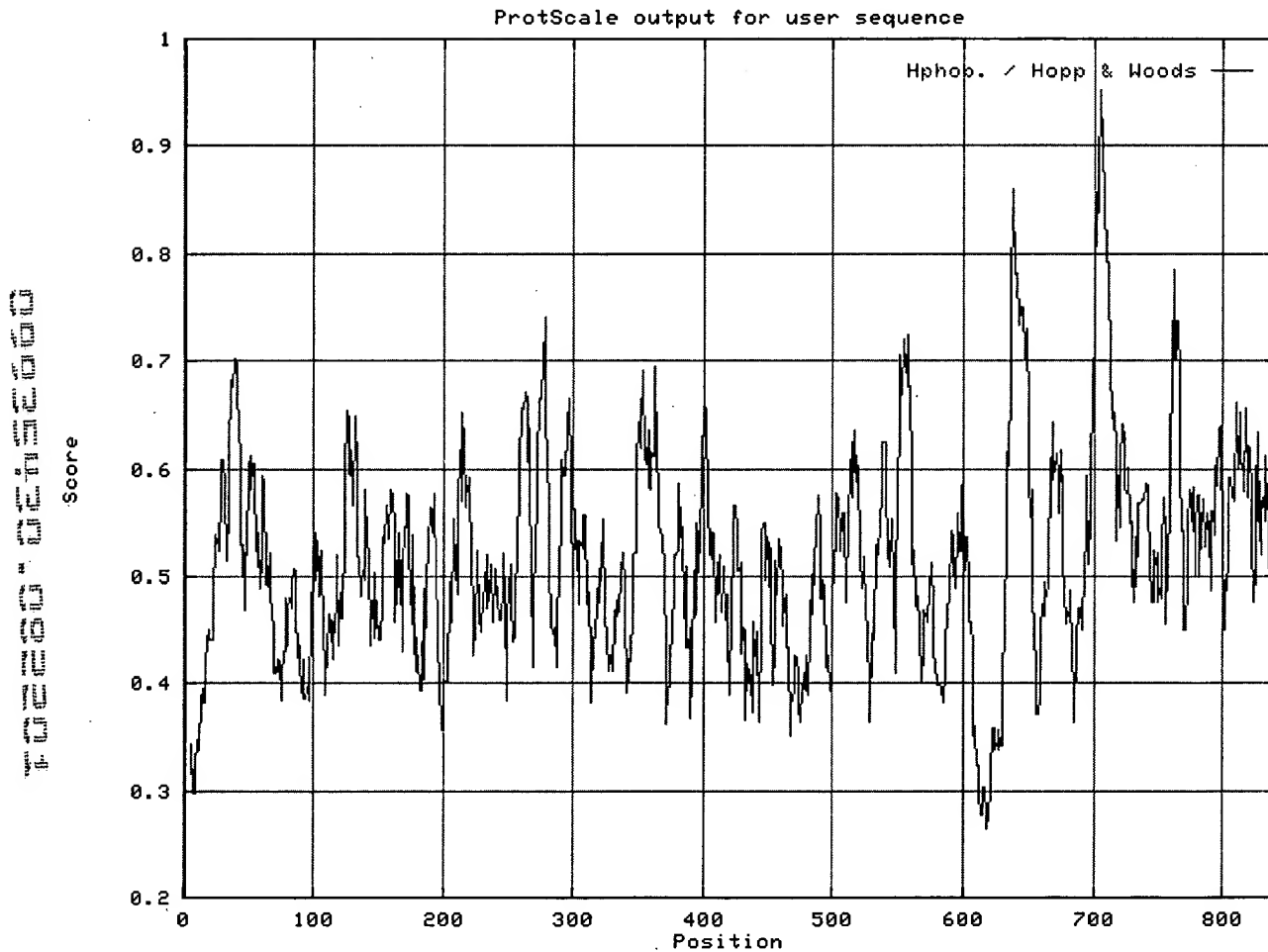


Figure 12. 158P1D7 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

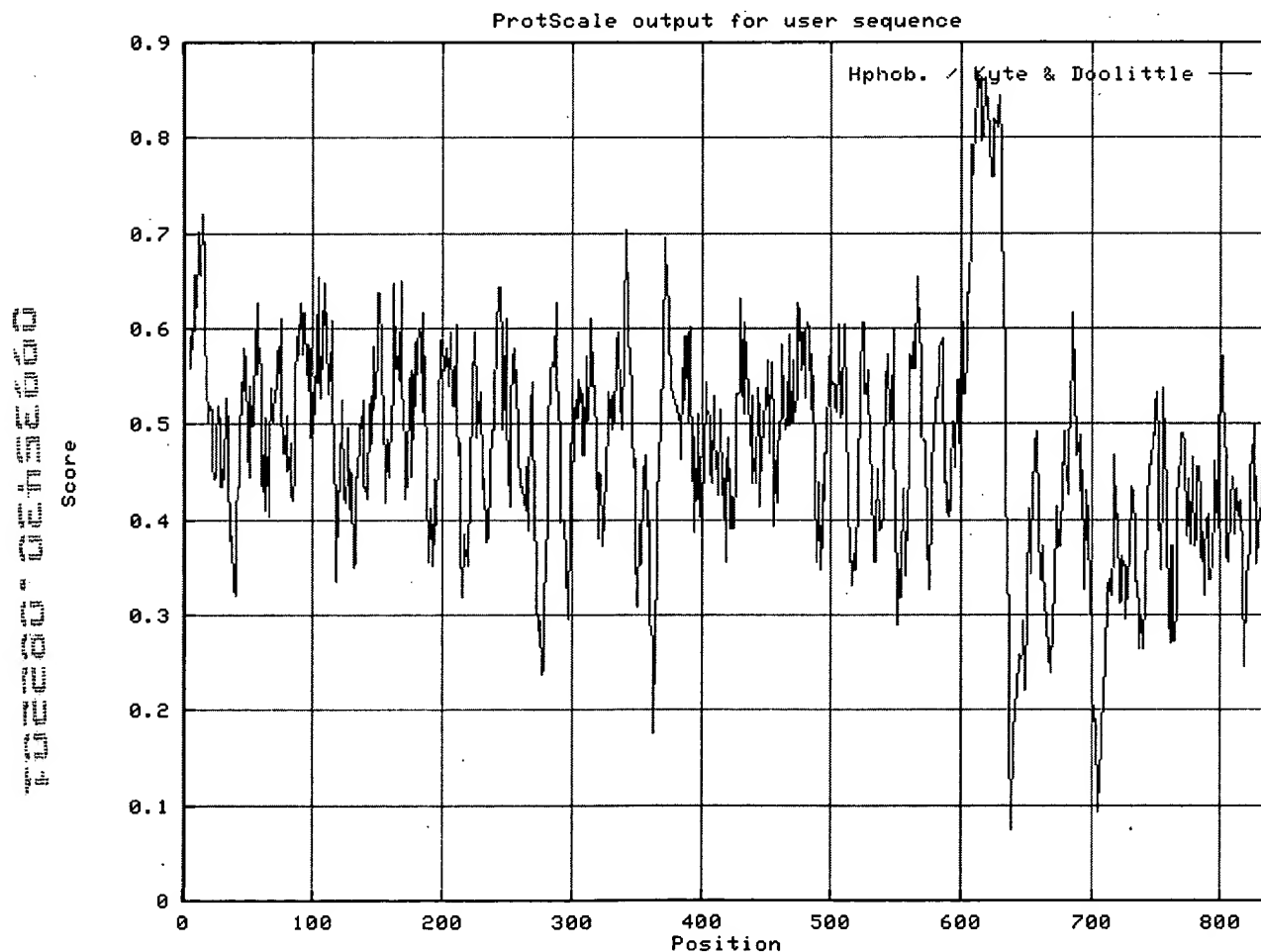


Figure 13. 158P1D7 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

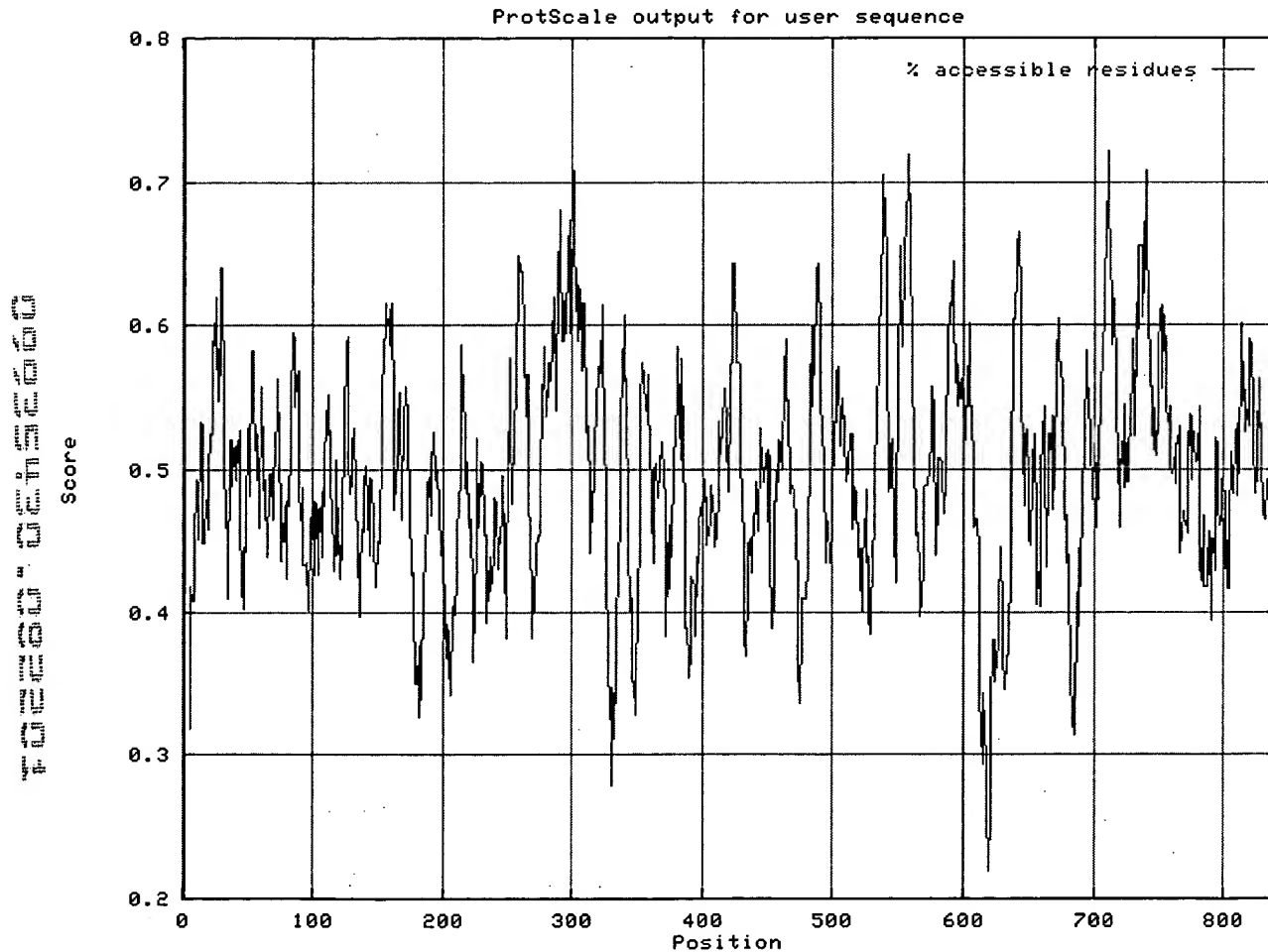


Figure 14. 158P1D7 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

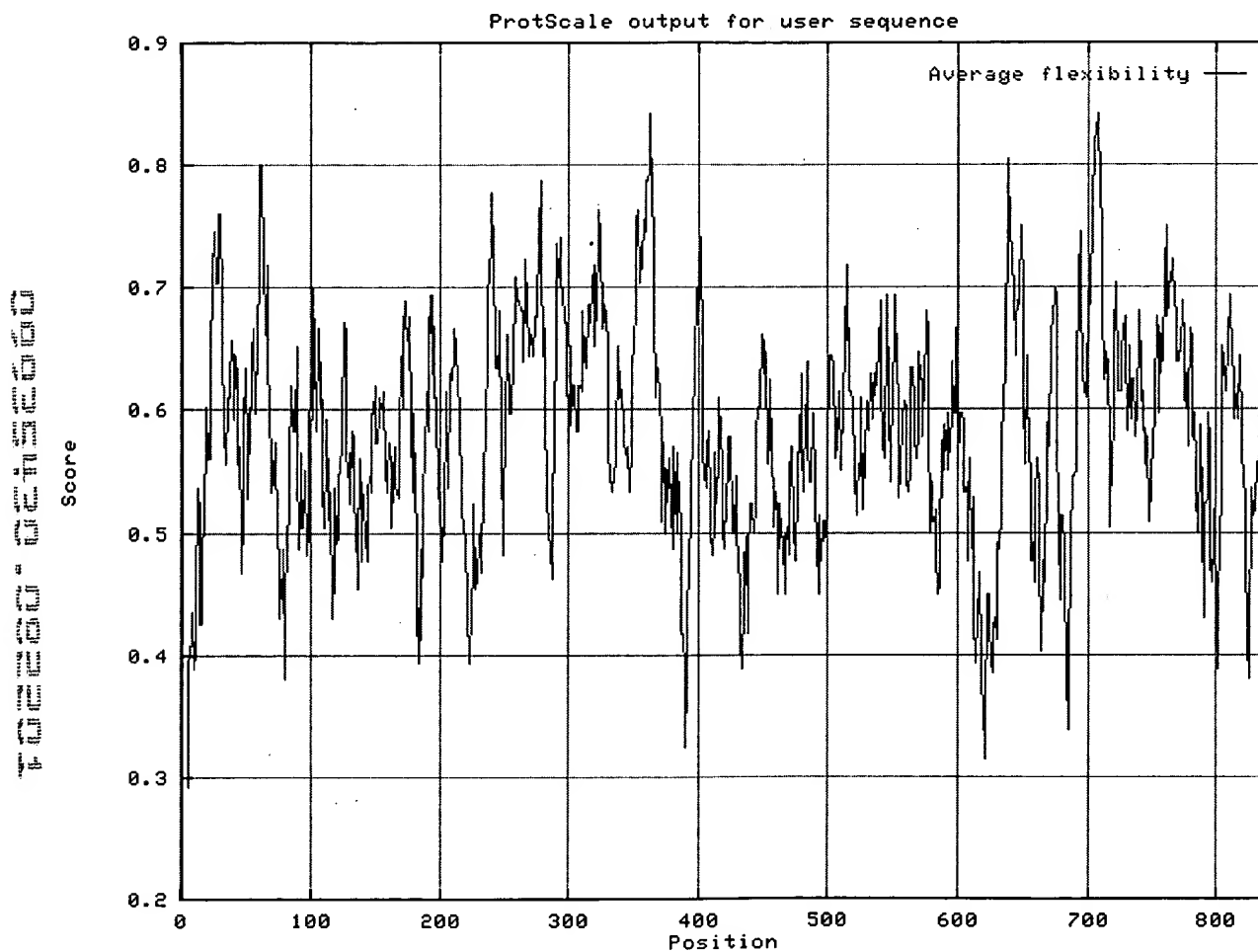
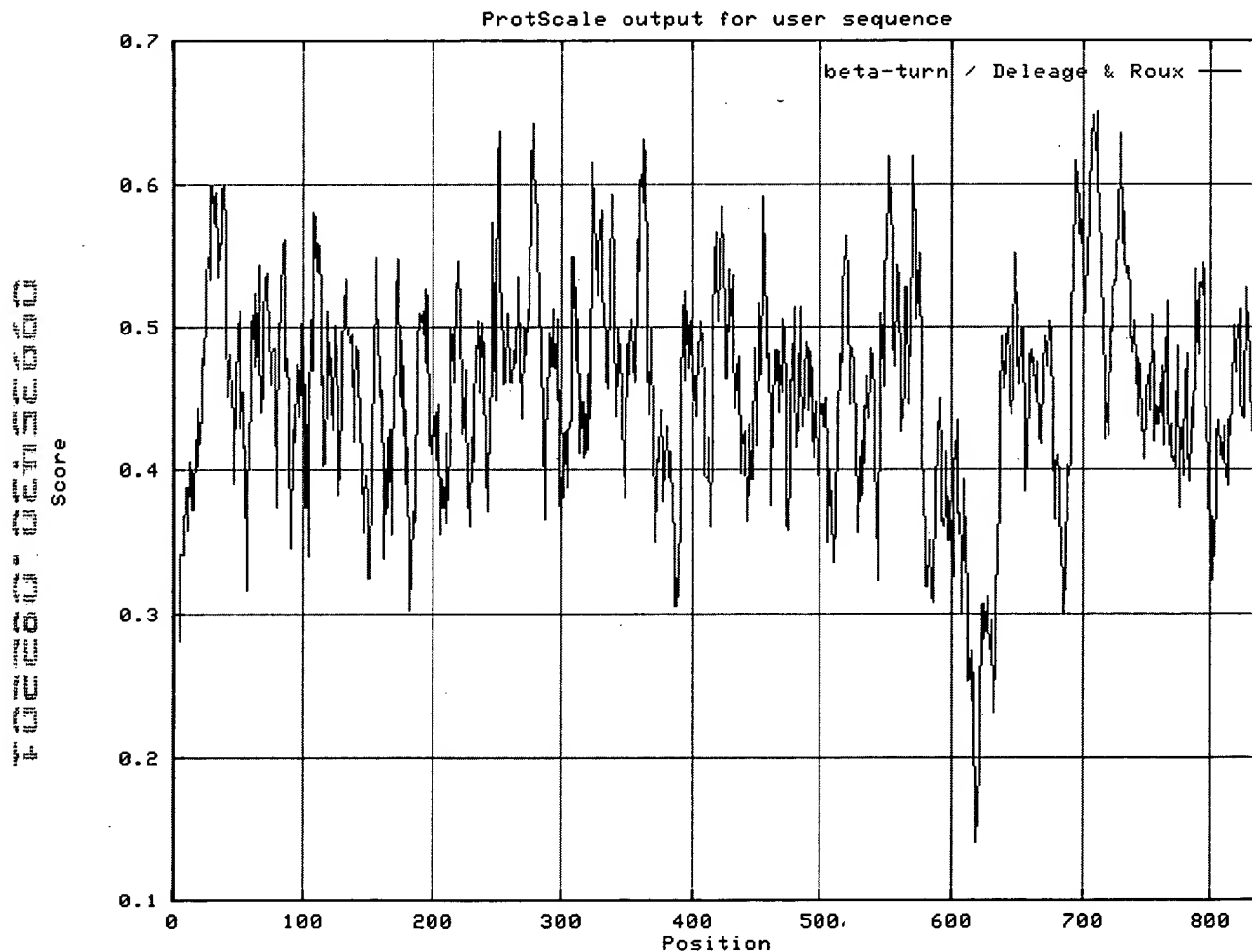
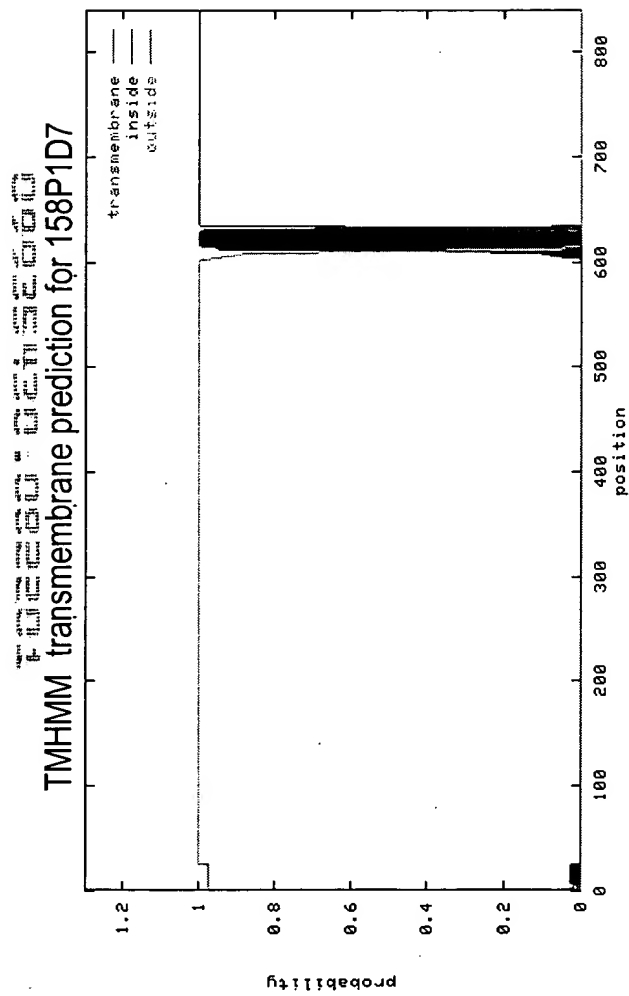


Figure 15. 158P1D7 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



16A



TMpred transmembrane prediction for 158P1D7

